

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 11.0727 Seconds

(without alignments)
977.656 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 1351

Sequence: 1 MGSLSRRKSLPSPLSSSV.....RESLSFYISLNDKAVSLDDA 261

Scoring table: BLOSUM62

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374.5	27.7	511	1 LYN_HUMAN	P07948 homo sapien
2	371.5	27.5	511	1 LYN_MOUSE	P25911 mus musculu
3	371.5	27.5	511	1 LYN_RAT	Q07014 rattus norv
4	364.5	27.0	526	1 HCK_HUMAN	P08631 homo sapien
5	362	26.8	504	1 HCK_MACA	Q95m30 macaca fasc
6	357.5	26.5	503	1 HCK_RAT	P50545 rattus norv
7	356.5	26.4	504	1 BLK_HUMAN	P51451 homo sapien
8	356	26.4	524	1 HCK_MOUSE	P08103 mus musculu
9	345.5	25.6	498	1 BLK_MOUSE	P16277 mus musculu
10	344	25.5	508	1 LCK_HUMAN	P06240 homo sapien
11	342.5	25.4	508	1 LCK_MOUSE	P06240 mus musculu
12	337	24.9	507	1 LCK_CHICK	P42683 gallus gall
13	337	24.9	507	1 LCK_MOUSE	P06240 mus musculu
14	321	23.8	541	1 YES_XENLA	P10936 xenopus lae
15	319.5	23.6	536	1 YES_CHICK	P09324 gallus gall
16	319.5	23.6	543	1 YES_HUMAN	P06241 homo sapien
17	316.5	23.4	529	1 FGR_HUMAN	P07947 homo sapien
18	315	23.3	544	1 YES_HUMAN	P09769 homo sapien
19	314.5	23.3	536	1 YES_XIPHE	P21447 xiphophorus
20	313	23.2	528	1 YES_XENLA	P14062 xenopus lae
21	313	23.2	533	1 FYN_MOUSE	P00528 rous sarcom
22	309.5	22.9	536	1 FYN_MOUSE	P00528 rous sarcom
23	309.5	22.9	541	1 YES_MOUSE	P39688 mus musculu
24	307	22.7	517	1 FGR_MOUSE	Q04736 mus musculu
25	305	22.6	535	1 YRK_CHICK	P14234 mus musculu
26	304	22.5	539	1 YES_CANFA	Q02977 gallus gall
27	301.5	22.3	533	1 FYN_CHICK	Q28923 canis fami
28	294	21.8	506	1 SRK_SPOLA	P05876 gallus gall
29	290.5	21.5	526	1 SRC_AYISR	P42690 spongilla 1
30	290.5	21.5	532	1 SRC_CHICK	P00523 avian sarco
31	290.5	21.5	552	1 SRC1_DROME	P00528 gallus gall
32	290.5	21.5	557	1 SRC1_AYISR	P14085 drosophila
33	290.5	21.5	587	1 SRC_AYISR	P15054 avian sarco

34	288.5	21.4	568	1 SRC_AYISR	P14084 avian sarco
35	281.5	20.8	535	1 SRC_RAT	Q9mnd3 rattus norv
36	280.5	20.8	526	1 SRC_XSVSR	P00524 rous sarcom
37	280.5	20.8	535	1 SRC_HUMAN	P12931 homo sapien
38	280	20.7	509	1 STR_HYDRA	P17713 hydra atten
39	278.5	20.6	531	1 SRC2_XENLA	P13116 xenopus lae
40	277.5	20.5	526	1 SRC_RSV	P00528 rous sarcom
41	275.5	20.4	540	1 SRC_MOUSE	P05480 mus musculu
42	273.5	20.2	531	1 SRC1_XENLA	P13115 xenopus lae
43	272.5	20.2	526	1 SRC_RSVH	P25020 rous sarcom
44	271	20.1	505	1 SRC1_SPOLA	P42686 spongilla 1
45	261	19.3	545	1 FGR_FSVGR	P00544 feline sarc

ALIGNMENTS

RESULT 1	ID	LYN_HUMAN	STANDARD;	PRT;	511 AA.
AC	P07948;				
DT	01-AUG-1988 (Rel. 08, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tyrosine-protein kinase LYN (EC 2.7.1.112).				
GN	LYN.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxId=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8712710; PubMed=3561390;				
RA	Matsumoto K., Fukushima S.-I., Senda K., Sukegawa J., Miyajima N.,				
RA	Yamanashi Y., Yamamoto T., Toyoshima K.;				
RT	"The yes-related cellular gene lyn encodes a possible tyrosine kinase				
RT	similar to p56lck.";				
RL	Mol. Cell. Biol. 7:237-243 (1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94171041; PubMed=8125304;				
RA	Rider L.G., Raben N., Miller L., Jelsma C.;				
RT	"The cdna encoding two forms of the lyn protein tyrosine kinase are				
RT	expressed in rat mast cells and human myeloid cells.";				
RL	Gene 138:219-222 (1994).				
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein				
CC	tyrosine phosphate.				
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;				
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC				
CC	SUBFAMILY.				
CC	-1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M16038; AAA59540.1; -				
DR	EMBL; M79321; AAB50019.1; -				
DR	PIR; A26719; TVHULY.				
DR	HSSP; P08631; IAD5.				
DR	Gene; H0NC:6735; LYN.				
DR	MTM; 165120; -				
DR	Interpro; IPR000719; Euk_pkinase.				
DR	Interpro; IPR000980; SH2.				
DR	Interpro; IPR001452; SH3.				
DR	Interpro; IPR001245; Tyr_kinase.				
DR	Pfam; PF00017; SH2, 1.				

DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR SMART; SMO0219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00002; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSELIC 22 42 MISSING (IN ISOPORN LYN B).
 SQ SUBSTANCE 511 AA; 58442 MW; 8419CD461204B364 CXC64;

Query Match 27.7%; Score 374.5; DB 1; Length 511;
 Best Local Similarity 40.3%; Pred. No. 1,8e-24;
 Matches 81; Conservative 36; Mismatches 75; Indels 9; Gaps 3;

QY 6 SRKSLPPSPSLSSVGGGVNMEABRSKATVALGSPGAGAEISRLGEPLTVSDE 65
 Db 37 SNKQRPVPE-SQLPGQRQCTDPEEGDITVALLYPDGHPDLSKKEKMKYLEEH 95
 QY 66 GDMWTVLSEVSGREYNIPSVHAKV---SHQWYEGSLSEKAEILLPNNPGAFILR 121
 Db 96 GEMWKAASLITKSGFIPSNVYAKLTETEWEFFKITRKAEEQLAPNSAGAFILR 155
 QY 122 ESQTRGSGYSLSVLRSPASMDIRHRYHICLDNGWYISPRTPPSIQALVDHPSLAD 181
 Db 156 ESETLKGSFSLVADPDVHGVDTIKYIKRSLDNGYIISPRTPPSIDMKRYQKQAD 215
 QY 182 DICCLIKPEPCVLRAGPLPGK 202
 Db 216 GLCRLEKACI---SPRPOK 232

RESULT 2

LYN_MOUSE

ID_LYN_MOUSE STANDARD; PRT; 511 AA.

AC P25911; Q62127;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9120688; PubMed=1710765;
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins";
 RL Mol. Cell. Biol. 11:3399-3406 (1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91203857; PubMed=2017160;
 RA Yi T., Bolen J.B., Ihle J.N.;
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21
 amino acids in the amino terminus";
 RL Mol. Cell. Biol. 11:2391-2398 (1991).
 RN [3]
 RP SEQUENCE OF 363-431 FROM N.A.
 RX MEDLINE=90152381; PubMed=2482828;
 RA Wilks A.F., Kujan R.R., Hovens C.M., Ralph S.J.;
 RT "The application of the polymerase chain reaction to cloning members
 of the protein tyrosine kinase family";
 RL Gene 85:67-74 (1989).
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOPORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; M64608; AAA39470.1; -;
 DR EMBL; M57696; AAA39471.1; -;
 DR EMBL; M57697; AAA39472.1; -;
 DR EMBL; M33426; AAA40017.1; -;
 DR PIR; A39719; A39719.
 DR HSSP; P08631; 1AD5.
 DR MGD; MGI:96892; LYN.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; TYR_kinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR SMART; SMO0219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00002; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPIC 24 44 MISSING (IN ISOFORM LYN B).
 FT CONFLICT 76 76 I -> F (IN REF. 2).
 FT CONFLICT 160 160 P -> L (IN REF. 2).
 FT CONFLICT 278 278 P -> L (IN REF. 2).
 FT CONFLICT 390 390 V -> I (IN REF. 2).
 FT CONFLICT 414 414 I -> F (IN REF. 3).
 FT CONFLICT 424 424 D -> N (IN REF. 1).
 FT CONFLICT 431 431 L -> P (IN REF. 3).
 SQ SEQUENCE 511 AA; 58661 MW; 393522CC90C5070 CRC64;
 Query Match 27.5%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 3.2e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 6 SRRKSLPSSLSVGGQGVMTAEERKATVAALGSPAGPAELSLRGEPLTISED 65
 DB 37 SNKQRPVPEF-HLPGQRFQTKDPEQSDIVVALYPDIGHDDLSFKKGEKMYLEH 95
 QY 66 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNGAFILR 121
 DB 96 GEMWKAJSSSKREGEFPENYAVAKNTLETETFEWFDITRDAERQLAPGNSAGAFILR 155
 QY 122 ESQTRRGYSLSVRLSPASMDRIRHRIHCLDNGWLYISPLTPEPLQALVDHYSELAD 181
 DB 156 ESETLKSFSLSVRDYDPMHGDVILKHKISLNDGCIYSIRITFPDISMIRKHQKQSD 215
 QY 182 DICCLKEPCVLOKAGPLPGK 202
 DB 216 GLCRRLERKACI---SPKPK 232
 RESULT 3
 LYN_RAT STANDARD; PRT; 511 AA.
 ID LYN_RAT
 AC 007014; 063320;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Minoguchi K., Nishikata H., Siraganian R.P.;
 RT "Bacterially expressed rat p56lyn binds several proteins in rat
 RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
 RT protein prominent in activated cells.";
 RL J. Immunol. 150:222-222(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97442484; PubMed=9295361;
 RA Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on LYN kinase for its constitutive
 RT association with the high affinity receptor for IgE.";
 RL J. Biol. Chem. 272:24072-24080(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC

CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; L14951; AAA1549.1; -;
 DR EMBL; L14782; AAA20944.1; -;
 DR EMBL; L14823; AAA20945.1; -;
 DR EMBL; AF000300; AAB71344.1; -;
 DR EMBL; AF000301; AAB71345.1; -;
 DR EMBL; AF000302; AAB71346.1; -;
 DR HSSP; P08631; IAD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00062; PKINASE; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00325; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00011; SH2; 1.
 DR PROSITE; PS0002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferrase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT_MET 0 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT DOMAIN 246 500
 FT NP_BIND 252 260
 FT BINDING 274 274
 FT ACT_SITE 366 366
 FT MOD_RES 396 396
 FT MOD_RES 507 507
 FT VARSPIC 24 44
 FT CONFLICT 230 230
 FT CONFLICT 307 307
 FT CONFLICT 418 418
 SQ SEQUENCE 511 AA; 58529 MW; 24A2B5E229CD43ED CRC64;
 Query Match 27.5%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 3.2e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 6 SRRKSLPSSLSVGGQGVMTAEERKATVAALGSPAGPAELSLRGEPLTISED 65
 DB 37 SNKQRPVPEF-HLPGQRFQTKDPEQSDIVVALYPDIGHDDLSFKKGEKMYLEH 95
 QY 66 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNGAFILR 121
 DB 96 GEMWKAJSSSKREGEFPENYAVAKNTLETETFEWFDITRDAERQLAPGNSAGAFILR 155
 QY 122 ESQTRRGYSLSVRLSPASMDRIRHRIHCLDNGWLYISPLTPEPLQALVDHYSELAD 181

DB 156 ESETLKGSFSLVDYDPMHGDVIMKHVIRSLNDNGYISPRITPCISDMIKHYKOSD 215
 OY 182 DICCLKEPCVLOAGAPLPCK 202
 DB 216 GICRLEKACT----SPKPK 232

RESULT 4
 ID_HCK_HUMAN STANDARD; PRT; 526 AA.
 AC P08631; O96CC0; O9HSY5; O9NUA4; O9UMJ5;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK and P60-HCK)
 DE Hemopoietic cell kinase.
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257942; PubMed=3496523;
 RA Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J.,
 RA le Beau M.M., Diaz M.O., Rowley J.D.;
 RT "Identification of a human gene (HCK) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells.";
 RL Mol. Cell. Biol. 7:2267-2275 (1987).
 RN [2]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., Marsh J.D., Lewis D.B., Perlmuter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hematopoietic origin.";
 RL Mol. Cell. Biol. 7:2267-2285 (1987).
 RN [3]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX TISSUE=ileal mucosa;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Ohtsuga T., Sugano S.;
 RT "MDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Mathewes L.H., Ashworth J., Burton J., Gilbert J.G.R.,
 RA Jones M., Scavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.W.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Dearden R., Dhand P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.U.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levensalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prachinangam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Senta H.K., Showken R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [6]
 RP SEQUENCE OF 179-526 FROM N.A.
 RX TISSUE=Spleen;
 RC MEDLINE=92241680; PubMed=1572549;
 RA Haderzky D., Streibhardt K., Ruesamen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
 RT exon-intron structure among human PTKs of the src family.";
 RL Gene 113:275-280 (1992).
 RN [7]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370 (1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 RX MEDLINE=97177106; PubMed=9024658;
 RA Sicheiri F., Moarefi I., Kuriyan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609 (1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 RX MEDLINE=96453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 RA Ladbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691 (1998).
 RN [10]
 RP STRUCTURE BY NMR OF 78-138.
 RX MEDLINE=98239731; PubMed=9571048;
 RA Horita D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 RA Gmeiner W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265 (1998).
 RN [11]
 RP STRUCTURE BY NMR OF 139-245.
 RX MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Gmeiner W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett. 406:131-135 (1997).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; P60-HCK (shown here) and P59-
 CC HCK, are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC *****
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CC EMBL, M16591; AAA52643.1; -
DR EMBL, M16592; AAA52644.1; -
DR EMBL, BC014435; AAH14435.1; -
DR EMBL, AK026432; BAB15482.1; -
DR EMBL, AL049539; CAB75606.1; -
DR EMBL, X58741; CAA41565.2; -
DR EMBL, X58742; CAA41565.2; JOINED.
DR EMBL, X58743; CAA41565.2; JOINED.
DR PIR, A27812; TYRHC.
DR PDB, 2HCK; 20-AUG-97.
DR PDB, 3HCK; 15-OCT-97.
DR PDB, 4HCK; 17-JUN-98.
DR PDB, 5HCK; 17-JUN-98.
DR PDB, 1AD5; 15-MAY-98.
DR PDB, 1BUI; 11-NOV-98.
DR Genew; HGNC:4840; HCK.
DR MIM, 142370; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR Pfam; PF00069; pkinase; 4.
DR Prodom; PD000066; SH3; 1.
DR Prodom; PD000093; SH2; 1.
DR Prodom; PD000252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00220; S_TGc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00002; SH2; 1.
DR PROSITE; PS00001; SH3; 1.
DR Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain; Alternative initiation;
KW 3D-structure.
FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.
FT CHAIN 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
FT INIT MET 22 22 FOR ISOFORM P59-HCK.
FT DOMAIN 78 138 SH3.
FT DOMAIN 144 241 SH2.
FT NP_BIND 268 276 PROTEIN KINASE.
FT BINDING 290 290 ATP.
FT ACT SITE 381 381 MYRISTATE (BY SIMILARITY).
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT MOD_RES 23 23 PHOSPHORYLATION (AUO-) (BY SIMILARITY).
FT CONFLICT 24 24 C -> S (IN REF. 1).
FT CONFLICT 144 144 W -> R (IN REF. 4).
SQ SEQUENCE 526 AA; 59599 MW; 8478877A0A641725 CRC64;
Query Match 27.0%; Score 364.5; DB 1; Length 526;
Best Local Similarity 42.2%; Pred. No. 1,3e-23;
Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 128 GSYSLSVRLSPASWDRIHRYRTHCLDNGMVLSPRLTSPSLQALVDHYSELDICLL 187
DB 178 GSYSLSVRLSPASWDRIHRYRTHCLDNGMVLSPRLTSPSLQALVDHYSELDICLL 237
QY 188 KPCPV 192
DB 238 SVPCM 242
RESULT 5
HCK_MACFA STANDARD; PRT; 504 AA.
ID HCK_MACFA
AC 095H30.02 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.12) (P56-HCK) (Hemopoietic cell
kinase).
DE HCK.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Picard C.;
RL Thesis (2001), University of Marseille, France.
CC - FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC - SUBCELLULAR LOCATION: Membrane-associated (By similarity). SRC
CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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FT  MOD RES 389 389 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ  SEQUENCE 504 AA; 57096 MW; 53829322D2DE3423 CRC64;

Query Match
Best Local Similarity 26.8%; Score 362; DB 1; Length 504;
Matches 73; Conservative 29; Mismatches 53; Indels 4; Gaps 1;

OY 38 VALGSPAGPAELSLRLGEPPLTIVSEGDWMTVLSEVSGREXNIPSVHAKV-----SHG 93
DB 62 VALYDEAIHHEHEDLSFGKGDQWVLEESGEWMMKARSLATKEGYIPSNVAVRDSLETET 121
OY 94 WLVEGLSRKAEELLPLPGNGAPFLRESQTRGSGYSLSVRLSPASWDRIRHRIHCL 153
DB 122 WFKGSRKDAEROLLPAGMGLSFWIDSETTGSGYSLSVRDYPDQGDVVKYKIRTL 181
OY 154 DNGWLYISPRLTFFSLDALVDHYSELADICLLKEPCV 192
DB 182 DNGGFYISPRSTFSTLQELVDHYKKGSDGLCKRLSVPCV 220

RESULT 6
HCK_RAT STANDARD; PRT; 503 AA.
AC P50545; O64647;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P55-HCK) (Hemopoietic cell
DE kinase).
GN HCK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92109719; PubMed=1764064;
RA Okano Y., Sugimoto Y., Fukuoka M., Matsui A., Nagata K.I., Nozawa Y.;
RT "Identification of rat cDNA encoding hck tyrosine kinase from
RT megakaryocytes.";
RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Master; TISSUE=Spleen;
RA Vijaya Gouri B.S., Rema V., Kamathkar S., Swarnp G.;
RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT characterization of its gene product.";
RL J. Biocel. 19:117-129(1994).
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC CONTRIBUTE TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC DEGRANULATE PROCESS OF NEUTROPHILS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S74141; AAB20754.1; -
DR EMBL; M83666; AAA41312.1; -
DR EMBL; X62345; CAA44218.1; -
DR HSSP; P08631; 1BUI.
DR Interpro; IPR000719; Euk_pkinase.

DR Interpro; IPR000980; SH2.
DR Interpro; IPR001452; SH3.
DR Interpro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SMO0252; SH2; 1.
DR SMART; SMO0326; SH3; 1.
DR SMART; SMO0219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50002; SH2; 1.
DR PROSITE; PS50001; SH3; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain.
FT DOMAIN 55 115
FT DOMAIN 121 218
FT DOMAIN 239 492
FT NP_BIND 245 253
FT BINDING 267 267
FT ACT_SITE 358 358
FT LIPID 2 2
FT MOD_RES 388 388
FT CONFUCT 51 51
FT CONFLICT 205 205
FT CONFLICT 306 306
SQ SEQUENCE 503 AA; 57016 MW; AIFCF3F0E82FF73 CRC64;

Query Match
Best Local Similarity 26.8%; Score 357.5; DB 1; Length 503;
Matches 86; Conservative 36; Mismatches 76; Indels 31; Gaps 5;

OY 1 MGSLPSR-RKSLPSPSSVGGGPGVME-----AESKAT-A 37
DB 1 MGCVSRFLRSGSKSKIERPNAQGPVVPDPSPKGLGPNINSLPGEVGESEDTIV 60
OY 38 VALGSPAGPAELSLRLGEPPLTIVSEGDWMTVLSEVSGREXNIPSVHAKV-----SHG 93
DB 61 VALYDEAIHHEHEDLSFGKGDQWVLEESGEWMMKARSLATKEGYIPSNVAVRDSLETET 120
OY 94 WLVEGLSRKAEELLPLPGNGAPFLRESQTRGSGYSLSVRLSPASWDRIRHRIHCL 153
DB 121 WFKGSRKDAEROLLPAGMGLSFWIDSETTGSGYSLSVRDYPDQGDVVKYKIRTL 180
OY 154 DNGWLYISPRLTFFSLDALVDHYSELADICLLKEPCVLOPAGLPCK 202
DB 181 DSGGFYISPRSTFSTLQELVDHYKKGSDGLCKRLSVPCV-----SPKPK 225

RESULT 7
BLK_HUMAN STANDARD; PRT; 504 AA.
AC P51451; O16291;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
DE BLK).
GN BLK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95123078; PubMed=7822795;

```

RA Islah K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.
 RT "Molecular cloning, characterization, and chromosomal localization of
 RT a human lymphoid tyrosine kinase related to murine Btk."
 RL J Immunol. 154:1265-1272(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95148218; PubMed=7845672;
 RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
 RA Niederhuber J.E.;
 RT "Molecular cloning and chromosomal localization of the human homologue
 RT of a B-lymphocyte specific protein tyrosine kinase (btk)."
 RL Oncogene 10:447-466(1995).
 CC -1- FUNCTION: BTK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTRAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 CC EMBL/ 23198; CAAB3965.1; -;
 DR EMBL/ S7617; AAB3365.1; -;
 DR HSSP/ P16277; BLK.
 DR Genew; HGNC:1057; BLK.
 DR MIM; 191305; -;
 DR InterPro; IPR000719; Euk_Dkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00011; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain.
 FT INIT MET 0
 FT LIPID 1
 FT DOMAIN 57 117 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 123 219 SH3.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP_BIND 246 254 ATP (BY SIMILARITY).
 FT BINDING 268 268 ATP (BY SIMILARITY).
 FT ACT_SITE 359 359 ATP (BY SIMILARITY).
 FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 286 286 M -> V (IN REF. 2).
 FT CONFLICT 406 406 I -> V (IN REF. 2).
 SQ SEQUENCE 504 AA; 57607 MW; BDDIDP50IC7370C8 CRC64;

Query Match 26.4%; Score 356.5; DB 1; Length 504;
 Beac Local Similarity 44.2%; Pred. No. 6e-23;
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

 QY 25 PVTMEARESKATVALGSPFAGAPAEISLRLCEPLTVSSDGDGMWTVLSEVSGREYNIPS 84
 DB PPDEHDEDKHVVGLDYDTAMNDRLQWLKKEKQLVLTCKGTGDMWLARSLVYTGREGVPS 109
 QY 85 VHVAKVS---HGVIYEGLSREKAEELLPLPENGGAFLIRRESQTRGSGSYLSRLSRPA 140
 DB 110 NFAVARESLMEHMFRRSGQKAEARQLAPINRAAGSLIRBSSTKGAFLSLVAK-DVTT 168
 QY 141 SWDIRHYRIHCLDNGMLYISPLTPPSLQALVDHYSELADICLLKEPCV 192
 DB 169 QGELIKHYRIKRLDEGGYISPLTPPSLQALVHYSEKKGDLQGLTLPCV 220
 RESULT 8
 HCK_MOUSE
 ID HCK_MOUSE STANDARD; PRT; 524 AA.
 AC P08103;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)
 GN (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BTK).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 22-524 FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=88067781; PubMed=3684607;
 RA Klemz M.J., Mckercher S.R., Maki R.A.;
 RT "Nucleotide sequence of the mouse hck gene";
 RL Nucleic Acids Res. 15:9600-9600(1987).
 RN [2]
 RP SEQUENCE OF 22-524 FROM N.A.
 RX MEDLINE=88068587; PubMed=3317404;
 RA Holtzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=9142636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: IP59-HCK (shown here) and P56-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTRAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
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CC EMBL, Y00487, CAA6544.1; -
 CC EMBL, J03023, AAA37305.1; -
 DR PIR, A27282, TWSHC.
 DR PIR, A3973, A3973.
 DR HSP, P08631, IAD5.
 DR MGD, MGI:96052, Hck.
 DR InterPro: IPR000719, Euk_pkinase.
 DR InterPro: IPR000980, SH2.
 DR InterPro: IPR001452, SH3.
 DR InterPro: IPR001245, Tyr_kinase.
 DR Pfam, PF00017, SH2_1.
 DR Pfam, PF00018, SH3_1.
 DR Pfam, PF00069, pkinase, 1.
 DR PRINTS, PR00401, SH2DOMAIN.
 DR PRINTS, PR00452, SH3DOMAIN.
 DR PRINTS, PR00109, TYRKINASE.
 DR ProDom, PD000001, Euk_pkinase, 1.
 DR ProDom, PD000065, SH3_1.
 DR ProDom, PD000093, SH2_1.
 DR SMART, SM00252, SH2_1.
 DR SMART, SM00326, SH3_1.
 DR SMART, SM00219, TYKc, 1.
 DR PROSITE, PS00107, PROTEIN_KINASE_ATP, 1.
 DR PROSITE, PS00109, PROTEIN_KINASE_TYR, 1.
 DR PROSITE, PS50011, PROTEIN_KINASE_DOM, 1.
 DR PROSITE, PS50002, SH2_1.
 DR PROSITE, PS50001, SH3_1.
 DR Tyrosinase, Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation.
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT INIT MET 22 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT DOMAIN 76 136 SH3.
 FT DOMAIN 142 239 FOR ISOFORM P56-HCK.
 FT DOMAIN 260 513 PROTEIN KINASE.
 FT NP_BIND 266 274 ATP (BY SIMILARITY).
 FT BINDING 288 288 ATP (BY SIMILARITY).
 FT ACT_SITE 379 379 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT SEQUENCE 524 AA; 59129 MW; D72FD69B38C9706 CRC64;

Query Match 26.4%; Score 356; DB 1; Length 524;
 Best Local Similarity 41.5%; Pred. No. 7e-23; 72; Indels 12; Gaps 4;
 Matches 83; Conservative 33; Mismatches 72;

QY 11 LPSPSSSSVGGPVTME---AERSKAT-AVALGSPAGPAELSLRLGEPITVSEEG 66
 DB 51 VPDPTSSSLGPNNSNMPGFEVGESEDTIVVALDYEAHREDLSFGQGMVLEENG 110
 QY 67 DMWTVLSEVSGRENTISVAVAV---SHMKEGSRKKEELLRLGPGAPFLIRE 122
 DB 111 EWMKARSLATKKEGYPSNVAVANSLTEEFKSRKDRHLLPGLMLSEFIND 170
 QY 123 SOTRSGSYSLVRLSRPASWDRIRHYRIHCLDNGLYISRLTPSLQALVDHYSELAAD 182
 DB 171 SETTKGYSLSVRDPDQHDGVTKHYKIRTLDSGFGYISRPSFSLDELVLHYKKKGK 230
 QY 183 ICCLLEKPCVLRAGPLPK 202
 DB 231 LCQKLSVPCV---SPKPK 246

RESULT 9
 BLK_MOUSE STANDARD; PRT; 498 AA.
 AC P16277,
 DT 01-AUG-1990 (rel. 15, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)

DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE BLK).
 GN BLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=90117147; PubMed=2404338;
 RA Dymekci S.M., Niederhuber J.E., Desiderio S.V.;
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
 RT cells.";
 RL Science 247:332-336(1990).
 RN [2]
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=96224819; PubMed=8639560;
 RA Metzler W.J., Lelting B., Pryor K., Mueller L., Farmer B.T. II;
 RT "The three-dimensional solution structure of the SH2 domain from
 RT p55blk kinase.";
 RL Biochemistry 35:6201-6211(1996).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC -1- IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@lsb-sib.ch).
 CC
 DR EMBL, M30903, AAA0453.1; -
 DR PIR, A40092, A40092.
 DR PDB, 1BLJ, 12-MAR-97.
 DR PDB, 1BLK, 12-MAR-97.
 DR MGD, MGI:88169, BLK.
 DR InterPro: IPR000719, Euk_pkinase.
 DR InterPro: IPR000980, SH2.
 DR InterPro: IPR001452, SH3.
 DR InterPro: IPR001245, Tyr_pkinase.
 DR Pfam, PF00017, SH2_1.
 DR Pfam, PF00018, SH3_1.
 DR Pfam, PF00069, pkinase, 1.
 DR PRINTS, PR00401, SH2DOMAIN.
 DR PRINTS, PR00452, SH3DOMAIN.
 DR PRINTS, PR00109, TYRKINASE.
 DR ProDom, PD000001, Euk_pkinase, 1.
 DR ProDom, PD000065, SH3_1.
 DR ProDom, PD000093, SH2_1.
 DR SMART, SM00252, SH2_1.
 DR SMART, SM00326, SH3_1.
 DR SMART, SM00219, TYKc, 1.
 DR PROSITE, PS00107, PROTEIN_KINASE_ATP, 1.
 DR PROSITE, PS00109, PROTEIN_KINASE_TYR, FALSE_NEG.
 DR PROSITE, PS50011, PROTEIN_KINASE_DOM, 1.
 DR PROSITE, PS50001, SH2_1.
 DR PROSITE, PS50002, SH3_1.
 DR Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; 3D-structure.
 FT INIT MET 0 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 51 111 SH3.
 FT DOMAIN 117 213 PROTEIN KINASE.
 FT NP_BIND 240 248 ATP (BY SIMILARITY).

FT BINDING 262 262 ATP (BY SIMILARITY).
 FT ACT SITE 353 353 BY SIMILARITY.
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 498 AA, 56513 MW, 849780.9 FPD577 CRC64;
 Query Match 25.6%, Score 345.5; DB 1; Length 498;
 Best Local Similarity 40.5%, Pred. No. 5.1e-22;
 Matches 75; Conservative 29; Mismatches 64; Indels 17; Gaps 3;
 QY 12 PPSPLSSVGGGCPVTMEKRSKATAVAGSPAGPAELSLRGEPLTVSSDDQMTV 71
 DB 43 PSEN-----QDDEBERFVALVDYAAVNDRLQVLGKQLQVLSGTDWMLA 90
 QY 72 LSEVSGREYNIPSVHAKVS---HGLVYEGLSREKAEELLPLPGNPGAFLIRSEQTR 127
 DB 91 RSLVTGREGVPSNFVAPVETLEVKWFRTISRKDAERQLAPMNKAGSFLIRSESNK 150
 QY 128 GSYLSVRLSRPASMDRIIRYHICLNGMLYSPRLTFFPSLQMLVHVSLEADICLL 187
 DB 151 GAFSLSVK-DITTOGEVAKHKINSLDNGSYISPRITFTPLQALVQHSKGDGLCQKL 209
 QY 188 KPCPV 192
 DB 210 TLPCV 214
 RESULT 10
 LCK_HUMAN STANDARD; PRT; 508 AA.
 AC P06239; P07100; Q9NYT8; Q96DW4; Q13152; Q12850;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (P56-LCK)
 DE (LCK) (T cell-specific protein-tyrosine kinase).
 GN LCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89123626; PubMed=3265417;
 RA Perlmutter R.M., March J.D., Lewis D.B., Peet R., Ziegler S.F.,
 RA Wilson C.B.;
 RT "Structure and expression of lck transcripts in human lymphoid
 RT cells.";
 RL J. Cell. Biochem. 38:117-126(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87133831; PubMed=3493153;
 RA Koga Y., Caecia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
 RA Mak T.W.;
 RT "A human T cell-specific cDNA clone (Y116) encodes a protein with
 RT extensive homology to a family of protein-tyrosine kinases.";
 RL Eur. J. Immunol. 16:1643-1646(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90108697; PubMed=2558056;
 RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
 RA Benarous R.;
 RT "Structure of the human lck gene: differences in genomic organisation
 RT within src-related genes affect only N-terminal exons.";
 RL Gene 84:105-113(1989).
 RN [4]
 RP SEQUENCE FROM N.A., VARIANTS L-27; POKP-231 INS; V-352, L-446, AND
 RP PHOSPHORYLATION OF TYR-393 AND TYR-504.
 RC TISSUE=Leukemia;
 RX MEDLINE=94187714; PubMed=8135546;
 RA Wright D.D., Setton B.W., Kamps M.P.;
 RT "Oncogenic activation of the lck protein accompanies translocation of
 RT the lck gene in the human HS2 T-cell leukemia.";
 RL Mol. Cell. Biol. 14:2429-2437(1994).
 RN [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemic T-cell;
 RX MEDLINE=96085119; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.;
 RT "An aberrant lck mRNA in two human T-cell lines.";
 RL Biochim. Biophys. Acta 1264:168-172(1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20462621; PubMed=11009097;
 RA Boncristiano W., Matolini W.B., D'Elia M.M., Pacini S., Valensin S.,
 RA Olivieri C., Amadi A., Falini B., Dei Prete G., Telford J.L.,
 RA Baldari C.T.;
 RT "Defective recruitment and activation of ZAP-70 in common variable
 RT immunodeficiency patients with T cell defects.";
 RL Eur. J. Immunol. 30:2632-2638(2000).
 RN [8]
 RP SEQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Veilleux A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
 RT and other non-lymphoid human tumor cell lines.";
 RL Oncogene Res. 1:357-374(1987).
 RN [9]
 RP SEQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=87000726; PubMed=3489486;
 RA Trevillyan J.W., Lin Y., Chen S.D., Phillips C.A., Canna C.,
 RA Linna T.J.;
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
 RT p56LCK.";
 RL Biochim. Biophys. Acta 888:286-295(1986).
 RN [10]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89096891; PubMed=2850479;
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
 RT "Structure of the murine lck gene and its rearrangement in a murine
 RT lymphoma cell line.";
 RL Mol. Cell. Biol. 8:3058-3064(1988).
 RN [11]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89313764; PubMed=2787474;
 RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
 RA Miyamoto N.G., Mak T.W.;
 RT "Structure of the two promoters of the human lck gene: differential
 RT accumulation of two classes of lck transcripts in T cells.";
 RL Mol. Cell. Biol. 9:2173-2180(1989).
 RN [12]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Paten R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 RN [13]
 RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.;
 RT "The SH3 domain of p56Lck is involved in binding to
 RT phosphatidylinositol 3'-kinase from T lymphocytes.";
 RL Mol. Cell. Biol. 13:7408-7417(1993).
 RN [14]
 RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=95155308; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.;

```

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CC
DR EMBL: X13529; CAA31884.1; -
DR EMBL: M36881; AAA59502.1; -
DR EMBL: X04476; CAA28165.1; -
DR EMBL: X14055; CAA32211.1; -
DR EMBL: X14053; CAA32211.1; JOINED.
DR EMBL: X14054; CAA32211.1; JOINED.
DR EMBL: U07236; AAA18225.1; -.
Query Match 25.5%; Score 344; DB 1; Length 508;
Best Local Similarity 41.4%; Pred. No. 7, 1e-22;
Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2
QY QY 26 VTMEAEKSKAT-----AVALSGFPAGPALSLRLGEPLTVSDDDMMTVTVSEVSGRE 79
Dy Dy 48 VTYGSSNPSPSPLODNLVIALHSEPSHDGGLGFEKBOURLLEDSGEMKAOSSLTQGE 107
QY QY 80 VYRSYVAVKVS---HGMLEYSREKAEELLLPONGGAFLIRSGOTRRGSYSLSVR 135
Dy Dy 108 GGIPIENVAAKASLEPEPFMKSLSKOAEKQLLAPGNTHGSFLLIRSGESTAGSFSLVR 167
QY QY 136 LSRRPAMDRIRRHTRHCLDNGMWLYISPLRTPPSLQALVDHSEYELADIGCLLKEPVQVOR 195
Dy Dy 168 DFDONQGEVYKVKYKTRINDNGGEYISPRITPPGLHVLVRYHYNASDGLCTRLSRPQCTOK 227
RESULT 11
LCK_MOUSE STANDARD; PRT; 508 AA.
ID LCK_MOUSE P06240; Q61794; Q61795; Q62220;
AC P06240; Q61794; Q61795; Q62220;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (P56-LCK)
DE (LSK).
DE LCK OR LSK-T.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX 1)
SEQUENCE FROM N.A.
RA MEDLINE=86079521; PubMed=2416464;
RA Marsh J.D., Peet R., Krebs B.G., Perlmutter R.M.;
RA "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and
RT overexpressed in the murine T cell lymphoma LSIRa.",
RL Cell 43:393-404 (1985).
[2]
SEQUENCE FROM N.A.
RA MEDLINE=86146842; PubMed=3081833;
RA Voronova A.F., Sefton B.M.;
RA "Expression of a new tyrosine protein kinase is stimulated by
RT retrovirus promoter insertion.",
RL Nature 319:682-685 (1986).
[3]
SEQUENCE OF 1-34 FROM N.A.
RA MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
RA "Structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line.",
RL Mol. Cell. Biol. 8:3058-3064 (1988).
[4]
SEQUENCE OF 1-10 FROM N.A.
RA MEDLINE=88142833; PubMed=3501824;
RA Voronova A.F., Adler H.T., Sefton B.M.;
RA "Two lck transcripts containing different 5' untranslated regions are
RT present in T cells.",
RL Mol. Cell. Biol. 7:4407-4413 (1987).
[5]
MUTAGENESIS OF TYR-504.
RA MEDLINE=86248001; PubMed=3380790;
RA Amrein K.E., Sefton B.M.;

```


Db 211 ASDGCTKLSRPGCTQK 227

RESULT 12

LCK CHICK STANDARD; PRT; 507 AA.

AC P42683;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL).

GN LCK.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

RN [1]

RP SEQUENCE OF 1-88 FROM N.A.

RX MEDLINE=9218685; PubMed=1545804;

RA Chow L., Ratcliffe M., Veilleux A.;

RT "tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.";

RL Mol. Cell. Biol. 12:1226-1233(1992).

RN [2]

RP SEQUENCE OF 46-507 FROM N.A.

RX MEDLINE=86097370; PubMed=3321053;

RA Strethard K., Mullins J.I., Bruck C., Ruebner-Waigmann H.;

RT "Additional member of the protein-tyrosine kinase family: the src- and lck-related protooncogene c-tkl.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

DR EMBL; M85043; AAA49003.1; -

DR EMBL; J03579; AAA49081.1; ALT_INIT.

DR HSSP; P06239; 3LCK.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.

DR ProDom; PD000066; SH3; 1.

DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; TyKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE;

KW ATP-binding; MYRISTATE; SH2 domain; SH3 domain; Palmitate;

KW Lipoprotein.

FT INIT MET 0 0 PROBABLE.

FT LIPID 1 1 MYRISTATE (BY SIMILARITY).

FT LIPID 2 2 PALMITATE (BY SIMILARITY).

FT LIPID 4 4 PALMITATE (BY SIMILARITY).

FT LIPID 59 119 SH3.

FT DOMAIN 125 222 SH2.

FT DOMAIN 125 222 SH2.

FT DOMAIN 243 496 PROTEIN KINASE.

FT NP BIND 249 257 ATP (BY SIMILARITY).

FT BINDING 271 271 ATP (BY SIMILARITY).

FT ACT SITE 362 362 BY SIMILARITY.

FT MOD_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 392 392 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).

FT MOD_RES 503 503

FT FT

SQ SEQUENCE 507 AA; 58008 MW; BC93C4FA891B6170 CRC64;

Query Match 24.9%; Score 337; DB 1; Length 507;

Best Local Similarity 43.8%; Pred. No. 2.8e-21;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

QY 38 VALSGFAPGAPALSLRGEPLTIVSEDDMTVLSFVSGREYNIPSVHAKVS---HG 93

Db 65 VALDYEPHTDGLDGLKQGEKRLRVLESGBMRAOSLTGQEGILFHNFMVAVNSLEPEP 124

QY 94 WLVEGLSREKAEELLPLPGNGAFILRESQTRGSGYSLSVRLSPASWDRIIRYRIHCL 153

Db 125 WFFNLRKRAEERLLASGNTHGSFLLRESETSKSGYSLSVDFPDQNGETVAKYKIRNM 184

QY 154 DNGWLTPSPPTSPSLQALVDHSELAIDICLLKEPVLDLR 195

Db 185 DNGGYTSPRVTFSSLMELVEYISSSDGLCTRLEKPERCTQK 226

RESULT 13

ID YES_XENLA STANDARD; PRT; 537 AA.

AC P10336;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (661-YES) (C-YES).

GN YES.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89296347; PubMed=2472592;

RA Steele R.E., Irwin M.Y., Knudsen C.L., Collett J.W., Fero J.B.;

RT "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte.";

RL Oncogene Res. 4:223-233(1989).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

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DR EMBL: X14377; CAA32551.1;
DR PIR: S08517; S08517.
DR HSP: P00523; 2PTK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000066; SH3; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
  Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2
FT DOMAIN 85 146 SH3.
FT DOMAIN 152 249 SH2.
FT DOMAIN 271 524 PROTEIN_KINASE.
FT NP_BIND 277 285 ATP (BY SIMILARITY).
FT BINDING 299 299 ATP (BY SIMILARITY).
FT ACT_SITE 390 390 BY SIMILARITY.
FT MOD_RES 420 420 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 537 AA; 60357 MW; PF66F615940AC31B CRC64;

Query Match 23.9%; Score 323.5; DB 1; Length 537;
Best Local Similarity 33.6%; Pred. No. 4.3e-20;
Matches 85; Conservative 38; Mismatches 91; Indels 39; Gaps 7;

QY 38 VALGSPAGPAELSLRLGEPLTIVE-DGDMWTVLSEVSGREYNIPSVHAKV-----SH 92
DB 91 VALYDEARTTDSFRKGEFQIINNTGDMWEARSAATCKGCIYPSVYVAPADSIQAE 150
QY 93 GMLYEGLSREKAEELLIPNPGGATLIESQTRRGYSISVRLSPASWDRIR-----H 147
DB 151 EWFYFGKGRKDAERLLNPGNGRTFLVRESSETTGAYSLISIR-----DMDEVRGDMVKH 205
QY 148 YRIHCLDNGMLYISPLTLPSPALVDHYSELADICCLKEKCC-----VLORAGP 198
DB 206 YKIRKLDNGGYITTRAGFESLQKLVKHSSEHADGLCYRLITVCPSPVQOGLAKDAWE 265
QY 199 LFGKDIPLPYTVQR-----TPLNWKELDSSLLFSEAAATGEESLSEGLRES 244
DB 266 IPRESLRIDVKGQCGCEGEVWIGTNGTITKAIKTLKPTGTMPEAFLEQAQIMKMLRHDK 325
QY 245 L-SFYISLNDNAV 256
DB 326 LVPLVAVVSEPI 338

RESULT 14
YES_CHICK STANDARD; PRT; 541 AA.
AC P09324;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES)
DE (C-YES).
GN YES.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
CC NCB1_TaxID=9031;
OK [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89041591; PubMed=3054816;
RA Sudol M., Kiewietter C., Zhao Y.H., Dorai T., Wang L.H.,
RA Hanafusa H., Kiewietter C., Zhao Y.H., Dorai T., Wang L.H.,
RT "Nucleotide sequence of a cDNA for the chick yes proto-oncogene:
RT comparison with the viral yes gene."
RT Nucleic Acids Res. 16:9876-9876(1988).
RN [2]
RP REVISION TO 232.
RA Sudol M.;
RN Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney, and Brain.
RX MEDLINE=93096482; PubMed=1281306;
RA Marcelle C., Eichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo."
RL Oncogene 7:2479-2487(1992).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBRAMITY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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DB EMBL: X13207; CAA31595.1;
DB EMBL: X12461; CAA31002.1;
DB EMBL: X69695; CAA49365.1;
DB PIR: S03324; TVCHVS.
DB HSP: P00523; 2PTK.
DB InterPro: IPR000719; Euk_pkinase.
DB InterPro: IPR000980; SH2.
DB InterPro: IPR001452; SH3.
DB InterPro: IPR001245; Tyr_pkinase.
DB Pfam: PF00017; SH2; 1.
DB Pfam: PF00018; SH3; 1.
DB Pfam: PF00069; pkinase; 1.
DB PRINTS: PR00401; SH2DOMAIN.
DB PRINTS: PR00452; SH3DOMAIN.
DB PRINTS: PR00109; TYRKINASE.
DB ProDom: PD000001; Euk_pkinase; 1.
DB ProDom: PD000066; SH3; 1.
DB ProDom: PD000093; SH2; 1.
DB SMART: SM00252; SH2; 1.
DB SMART: SM00326; SH3; 1.
DB SMART: SM00219; TyrKc; 1.
DB PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DB PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DB PROSITE: PS50001; SH2; 1.
DB PROSITE: PS50002; SH3; 1.
KW Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2
FT LIPID 2
FT MYRISTATE (BY SIMILARITY).

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RX MEDLINE=93327750; PubMed=7687536;
 RA Noble M.E.M., Musacchio A., Saraste M., Courtneidge S.A.,
 RA Wierenga R.K.;
 RT "Crystal structure of the SH3 domain in human Fyn; comparison of the
 RT three-dimensional structures of SH3 domains in tyrosine kinases and
 RT spectrin.";
 RL EMBO J. 12:2617-2624(1993).
 RN [5]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 80-141.
 RX MEDLINE=95393198; PubMed=7664083;
 RA Musacchio A., Saraste M., Wilmanns M.;
 RA "High-resolution crystal structures of tyrosine kinase SH3 domains
 RT complexed with proline-rich peptides";
 RL Nat. Struct. Biol. 1:546-551(1994).
 RN [6]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 84-140 IN COMPLEX WITH NEF.
 RX MEDLINE=96279837; PubMed=8681387;
 RA Lee C.H., Sakseela K., Mirza U.B., Chait B.T., Kurtyan J.;
 RA "Crystal structure of the conserved core of HIV-1 Nef complexed with
 RT a Src family SH3 domain";
 RL Cell 85:931-942(1996).
 RN [7]
 RN STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=9639716; PubMed=8805547;
 RA Morton C.J., Pugh D.U.R., Brown E.L.J., Kahmann J.D., Renzoni D.A.C.,
 RA Campbell I.D.;
 RT "Solution structure and peptide binding of the SH3 domain from human
 RT Fyn.";
 RL Structure 4:705-714(1996).
 RN [8]
 RN STRUCTURE BY NMR.
 RX MEDLINE=97121261; PubMed=8961927;
 RA Renzoni D.A., Pugh D.J., Siligardi G., Das P., Morton C.J., Rossi C.,
 RA Waterfield J.D., Campbell I.D., Ladbury J.E.;
 RT "Structural and thermodynamic characterization of the interaction of
 RT the SH3 domain from Fyn with the proline-rich binding site on the p55
 RT subunit of p13-kinase.";
 RL Biochemistry 35:15646-15653(1996).
 RN [9]
 RN STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=98035454; PubMed=9351806;
 RA Mulhern T.D., Shaw G.J., Morton C.J., Day A.J., Campbell I.D.;
 RA "The SH2 domain from the tyrosine kinase Fyn in complex with a
 RT phosphotyrosyl peptide reveals insights into domain stability and
 RT binding specificity.";
 RL Structure 5:1313-1323(1997).
 RN [10]
 RN BINDING OF SH3 DOMAIN TO PI 3-KINASE.
 RX MEDLINE=93348274; PubMed=8394019;
 RA Praad K.V., Janssen O., Kapeller R., Raab M., Cantley L.C.;
 RA Rudak C.E.;
 RA "Src-homology 3 domain of protein kinase p55fyn mediates binding to
 RT phosphatidylinositol 3-kinase in T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7366-7370(1993).
 CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P55 SUBUNIT OF
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING
 CC PROTEIN (FEB).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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